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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=12; day=16; hr=15; min=39; sec=26; ms=904;
]

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Application No: 10593567

Version No: 1.0

Input Set:

Output Set:

Started: 2008-12-01 16:03:08.543

Finished: 2008-12-01 16:03:09.613

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 70 ms

Total Warnings: 9

Total Errors: 0

No. of SeqIDs Defined: 13

Actual SeqID Count: 13

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |

SEQUENCE LISTING

<110> GROGER, HARALD
 WERNER, HELGE
 ALTENBUCHNER, JOSEF
 MENZEL, ANNE
 HUMMEL, WERNER

<120> PROCESS FOR PREPARING OPTICALLY ACTIVE AMINO ACIDS USING A
 WHOLE-CELL CATALYST

<130> 294227US-10757-9350-0-X PCT

<140> 10593567

<141> 2008-12-01

<150> PCT/EP2005/002933

<151> 2005-03-18

<150> DE 102004014280.7

<151> 2004-03-22

<160> 13

<170> PatentIn version 3.5

<210> 1

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 1

aaaaaactta agaaggagat atacatatga cattagaaat cttcgaa

47

<210> 2

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 2

aaaaaactgc agttagcgac ggctaataat at

32

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 3
aaaaaacata tgaagattgt cttagttctt 30

<210> 4
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 4
aaaaaagacg tcttatttct tatcgtgttt acc 33

<210> 5
<211> 1120
<212> DNA
<213> Bacillus cereus

<220>

<221> CDS
<222> (20)..(1120)

<400> 5
ttaagaagga gatatacat atg aca tta gaa atc ttc gaa tac tta gaa aaa 52
Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys
1 5 10

tat gat tat gag caa gta gta ttt tgt caa gat aaa gaa tct ggt tta 100
Tyr Asp Tyr Glu Gln Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu
15 20 25

aaa gca att att gca att cat gat aca aca ctt gga ccg gct ctt ggt 148
Lys Ala Ile Ile Ala Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly
30 35 40

gga aca aga atg tgg aca tat gat tct gaa gaa gcg gcg att gaa gat 196
Gly Thr Arg Met Trp Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp
45 50 55

gca ttg cgt ctt gca aaa ggg atg aca tac aaa aac gca gca gct ggt 244
Ala Leu Arg Leu Ala Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly
60 65 70 75

tta aac tta ggt ggt gcg aaa aca gta att atc ggt gat cct cgt aaa 292
Leu Asn Leu Gly Gly Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys
80 85 90

| | |
|---|------|
| gat aag agc gaa gca atg ttc cgt gca cta gga cgt tat atc caa gga | 340 |
| Asp Lys Ser Glu Ala Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly | |
| 95 100 105 | |
| cta aac gga cgt tac att aca gct gaa gat gtt ggt aca aca gta gat | 388 |
| Leu Asn Gly Arg Tyr Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp | |
| 110 115 120 | |
| gat atg gat att atc cat gaa gaa act gac ttt gta aca ggt atc tca | 436 |
| Asp Met Asp Ile Ile His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser | |
| 125 130 135 | |
| cca tca ttc ggt tct tct ggt aac cca tct ccg gta act gca tac ggt | 484 |
| Pro Ser Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly | |
| 140 145 150 155 | |
| gtt tac cgt ggt atg aaa gca gct gca aaa gaa gct ttc ggt act gac | 532 |
| Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp | |
| 160 165 170 | |
| aat tta gaa gga aaa gta att gct gtt caa ggc gtt ggt aac gta gca | 580 |
| Asn Leu Glu Gly Lys Val Ile Ala Val Gln Gly Val Gly Asn Val Ala | |
| 175 180 185 | |
| tat cac cta tgc aaa cat tta cac gct gaa gga gca aaa tta att gtt | 628 |
| Tyr His Leu Cys Lys His Leu His Ala Glu Gly Ala Lys Leu Ile Val | |
| 190 195 200 | |
| aca gat att aat aaa gaa gct gta caa cgt gct gta gaa gaa ttc ggt | 676 |
| Thr Asp Ile Asn Lys Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly | |
| 205 210 215 | |
| gca tca gca gtt gaa cca aat gaa att tac ggt gtt gaa tgc gat att | 724 |
| Ala Ser Ala Val Glu Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile | |
| 220 225 230 235 | |
| tac gca cca tgt gca cta ggc gca aca gtt aat gat gaa act att cca | 772 |
| Tyr Ala Pro Cys Ala Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro | |
| 240 245 250 | |
| caa ctt aaa gca aaa gta atc gca ggt tct gcg aat aac caa tta aaa | 820 |
| Gln Leu Lys Ala Lys Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys | |
| 255 260 265 | |
| gaa gat cgt cat ggt gac atc att cat gaa atg ggt att gta tac gca | 868 |
| Glu Asp Arg His Gly Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala | |
| 270 275 280 | |
| cca gat tat gta att aat gca ggt ggc gta att aac gta gca gac gaa | 916 |
| Pro Asp Tyr Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu | |
| 285 290 295 | |
| tta tat gga tac aat aga gaa cgt gca cta aaa cgt gtt gag tct att | 964 |
| Leu Tyr Gly Tyr Asn Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile | |
| 300 305 310 315 | |
| tat gac acg att gca aaa gta atc gaa att tca aaa cgc gat ggc ata | 1012 |

Tyr Asp Thr Ile Ala Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile
320 325 330

gca act tat gta gcg gca gat cgt cta gct gaa gag cgc att gca agc 1060
Ala Thr Tyr Val Ala Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser
335 340 345

ttg aag aat tct cgt agc act tac tta cgc aac ggt cac gat att att 1108
Leu Lys Asn Ser Arg Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile
350 355 360

agc cgt cgc taa 1120
Ser Arg Arg
365

<210> 6

<211> 366

<212> PRT

<213> Bacillus cereus

<400> 6

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1 5 10 15

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
20 25 30

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

| | | | |
|---|-----|-----|-----|
| Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met | | | |
| 145 | 150 | 155 | 160 |
| | | | |
| Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys | | | |
| 165 | 170 | 175 | |
| | | | |
| Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys | | | |
| 180 | 185 | 190 | |
| | | | |
| His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys | | | |
| 195 | 200 | 205 | |
| | | | |
| Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu | | | |
| 210 | 215 | 220 | |
| | | | |
| Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala | | | |
| 225 | 230 | 235 | 240 |
| | | | |
| Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys | | | |
| 245 | 250 | 255 | |
| | | | |
| Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly | | | |
| 260 | 265 | 270 | |
| | | | |
| Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile | | | |
| 275 | 280 | 285 | |
| | | | |
| Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn | | | |
| 290 | 295 | 300 | |
| | | | |
| Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala | | | |
| 305 | 310 | 315 | 320 |
| | | | |
| Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala | | | |
| 325 | 330 | 335 | |
| | | | |
| Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg | | | |
| 340 | 345 | 350 | |
| | | | |
| Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg | | | |
| 355 | 360 | 365 | |

<210> 7
<211> 1095
<212> DNA
<213> *Candida boidinii*

<220>
<221> CDS
<222> (1)..(1095)

<400> 7
atg aag att gtc tta gtt ctt tat gat gct ggt aag cac gct gct gat 48
Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
1 5 10 15

gaa gaa aaa tta tat ggt tct act gaa aat aaa tta ggt att gct aat 96
Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn
20 25 30

tgg tta aaa gat caa ggt cat gaa cta att act act tct gat aaa gaa 144
Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
35 40 45

ggt gaa aca agt gaa ttg gat aaa cat atc cca gat gct gat att atc 192
Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile
50 55 60

atc acc act cct ttc cat cct gct tat atc act aag gaa aga ctt gac 240
Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
65 70 75 80

aag gct aag aac tta aaa tta gtc gtt gtc gct ggt gtt ggt tct gat 288
Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
85 90 95

cac att gat tta gat tat att aat caa aca ggt aag aaa atc tca gtc 336
His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
100 105 110

ctg gaa gtt aca ggt tct aat gtt gtc tct gtt gct gaa cac gtt gtc 384
Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
115 120 125

atg acc atg ctt gtc ttg gtt aga aat ttc gtt cca gca cat gaa caa 432
Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
130 135 140

att att aac cac gat tgg gag gtt gct gct atc gct aag gat gct tac 480
Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
145 150 155 160

gat atc gaa ggt aaa act atc gct acc att ggt gct ggt aga att ggt 528
Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
165 170 175

tac aga gtc ttg gaa aga tta ctc cca ttt aat cca aaa gaa tta tta 576
Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu

| 180 | 185 | 190 | |
|---|-----|-----|------|
| tac tac gat tat caa gct tta cca aaa gaa gct gaa gaa aaa gtt ggt | | | 624 |
| Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly | | | |
| 195 | 200 | 205 | |
| gct aga aga gtt gaa aat att gaa gaa tta gtt gct caa gct gat atc | | | 672 |
| Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile | | | |
| 210 | 215 | 220 | |
| gtt aca gtt aat gct cca tta cac gca ggt aca aaa ggt tta att aat | | | 720 |
| Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn | | | |
| 225 | 230 | 235 | 240 |
| aag gaa tta tta tct aaa ttt aaa aaa ggt gct tgg tta gtc aat acc | | | 768 |
| Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr | | | |
| 245 | 250 | 255 | |
| gca aga ggt gct att gct gtt gct gaa gat gtt gca gca gct tta gaa | | | 816 |
| Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu | | | |
| 260 | 265 | 270 | |
| tct ggt caa tta aga ggt tac ggt ggt gat gtt tgg ttc cca caa cca | | | 864 |
| Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro | | | |
| 275 | 280 | 285 | |
| gct cca aag gat cac cca tgg aga gat atg aga aat aaa tat ggt gct | | | 912 |
| Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala | | | |
| 290 | 295 | 300 | |
| ggg aat gcc atg act cct cac tac tct ggt act act tta gac gct caa | | | 960 |
| Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln | | | |
| 305 | 310 | 315 | 320 |
| aca aga tac gct gaa ggt act aaa aat att ttg gaa tca ttc ttt acc | | | 1008 |
| Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr | | | |
| 325 | 330 | 335 | |
| ggg aaa ttt gat tac aga cca caa gat att atc tta tta aat ggt gaa | | | 1056 |
| Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu | | | |
| 340 | 345 | 350 | |
| tac gtt act aaa gct tac ggt aaa cac gat aag aaa taa | | | 1095 |
| Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys | | | |
| 355 | 360 | | |

<210> 8

<211> 364

<212> PRT

<213> Candida boidinii

<400> 8

| | | | | | | | | | | | | | | | |
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| Met | Lys | Ile | Val | Leu | Val | Leu | Tyr | Asp | Ala | Gly | Lys | His | Ala | Ala | Asp |
| 1 | | | | 5 | | | | | 10 | | | | | | 15 |

Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn
20 25 30

Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
35 40 45

Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile
50 55 60

Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
65 70 75 80

Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
85 90 95

His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
100 105 110

Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
115 120 125

Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
130 135 140

Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
145 150 155 160

Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
165 170 175

Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu
180 185 190

Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly
195 200 205

Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile
210 215 220

Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
225 230 235 240

Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr

245

250

255

Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu
260 265 270

Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
275 280 285

Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
290